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GenCore version 5.1.6
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Om nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:18:03 ; Search time 1371.68 Seconds
(without alignment)
12007.805 Million cell updates/sec

Title: US-09-807-933B-8
Perfect score: 1017
Sequence: 1 atgaagtcacccgtgtctat.....caggttcgaaagaagtaa 1017

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
EST:
1: em_eacba:*
2: em_eacbm:*
3: em_eactm:*
4: em_eactm:*
5: em_eactm:*
6: em_eactm:*
7: em_eactm:*
8: em_eactm:*
9: gb_eactl:*
10: gb_eactl:*
11: gb_eactl:*
12: gb_eactl:*
13: gb_eactl:*
14: gb_eactl:*
15: em_eactm:*
16: em_eactm:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	173	17.0	691	10	BE585661 EST#6PSP6
2	122.2	12.0	450	13	BT2007229 BT2007229
3	111	10.9	444	13	BT190695 BT190695
4	104.4	10.3	426	13	BT187295 BT187295
5	81.2	8.0	215	13	BT190568 BT190568
6	73.6	7.2	989	17	CNS02HAA4 AL197365 Tetracodon

7	72	7.1	494	17	FR0048073	AL444858 Fugu rubr
8	70.8	7.0	350	17	BH879665	BH879665 hc47n12.9
9	70.6	6.9	450	17	FR0025683	AL018519 F. rubripes
10	70.6	6.9	501	17	FR0048173	AL444958 Fugu rubr
11	70	6.9	914	17	AZ205202	AZ205202 SP_0100_A
12	69.6	6.8	933	17	AZ204694	AZ204694 SP_0100_A
13	67.8	6.7	788	17	AZ183942	AZ183942 SP_1002_A
14	67.2	6.6	627	17	BH179321	BH179321 014_P_01-
15	67.2	6.6	627	17	CNS07LFL	AL616275 T7 end of
16	66	6.5	735	17	CNS07LFL	AL299119 Tetracodon
17	65.8	6.5	335	10	AW275677	AW275677 xp08e07.x
18	65.8	6.5	619	17	FR0047601	AL444386 Fugu rubr
19	65.6	6.5	570	17	AZ149014	AZ149014 SP_0020_B
20	65.2	6.4	530	17	AZ166409	AZ166409 SP_0088_A
21	64.8	6.4	392	17	FR0048008	AL444793 Fugu rubr
22	64.2	6.3	331	17	BH881398	BH881398 hv25c11.b
23	64.2	6.3	773	17	CNS01V7G	AL169549 Tetracodon
24	64	6.3	500	17	B67199	B67199 CpG0015B Cp
25	63.8	6.3	354	17	AQ935615	AQ935615 CpG2561B
26	63.4	6.2	250	17	BH878991	BH878991 hb85e08.b
27	63.2	6.2	824	13	AZ185454	AZ185454 SP_1005_A
28	62.6	6.2	522	13	BT783235	BT783235 K18909.Y
29	62.6	6.2	621	17	AZ164800	AZ164800 SP_0076_B
30	62.2	6.1	358	17	BH777606	BH777606 f2mb013f0
31	62.2	6.1	580	17	BH763893	BH763893 BMBAC314F
32	62	6.1	177	17	BH881173	BH881173 hv23q03.b
33	62	6.1	204	17	BH882682	BH882682 hv38h10.g
34	62	6.1	230	17	BH869848	BH869848 hm54h10.g
35	62	6.1	510	13	BT374789	BT374789 BT374789
36	62	6.1	619	17	FR0006944	290754 F. rubripes
37	62	6.1	810	17	AZ199472	AZ199472 SP_1039_B
38	61.8	6.1	218	17	BH875125	BH875125 hb83h02.g
39	61.2	6.0	795	17	AZ186967	AZ186967 SP_1008_A
40	60.6	6.0	454	17	AZ178507	AZ178507 SP_0161_B
41	60.2	5.9	976	17	CNS01FBX	AL141646 Anopheles
42	60	5.9	558	17	AZ146816	AZ146816 SP_0047_B
43	59.8	5.9	539	9	AT002510	AT002510 AT002510
44	59.6	5.9	485	13	BT370491	BT370491 BT370491
45	59.4	5.8	196	17	PR0047508	AL444293 Fugu rubr

ALIGNMENTS

RESULT 1
LOCUS BE585661
DEFINITION EST#6PSP6_D02_d2_014 KSU wheat Fusarium graminearum infected spike
CDNA library Trilicium aestivum CDNA clone EST#6PSP6_D02_d2_014,
mRNA sequence.
ACCESSION BE585661
VERSION BE585661.1 GI:9838604
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Trilicium aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 691)
Fellers,J.P., Li,W.L., Hill-Ambroz,K., Matthews,A. and Gill,B.S.
The structure and function of the expressed portion of the wheat
genomes - Kansas State University, Fusarium graminearum infected
spike CDNA library
Unpublished (2000)
Contact: John Fellers
US Department of Agriculture, Agriculture Research Service, Plant
Science and Entomology Unit
Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State
University, Manhattan, KS 66506, USA
Tel: 785-532-2367
Fax: 785-532-6167
Email: jpf@alfalfa.ksu.edu
Sequence have been trimmed to remove vector sequence and low

JOURNAL COMMENT

quality sequence with phred score less than 20
Seq primer: SP6.

FEATURES

Location/Qualifiers
1..691
/organism="Triticum aestivum"
/cultivar="Suma13"
/db xref="taxon:4565"
/clone="EST#6PSP6.D02.d2.014"
/clone.lib="KSU wheat Fusarium graminearum infected spike
cDNA library"
/cissue.type="Spike"
/dev stage="Adult plant"
/lab host="E. coli JM109"
/note="vector: pGEM-T easy; Site 1: SacI; Site 2: SpeI;
plants were grown in the greenhouse. Spikes were infected
with Fusarium graminearum (at what stage). Total RNA, and
poly(A) RNA were prepared from infected spikes. cDNA was
prepared using the SmartIT PCR cDNA synthesis kit from
Clontech. cDNA was cloned into the pGEM-T easy vector
from Promega."

BASE COUNT 135 a 196 c 163 g 197 t

ORIGIN

Query Match 17.0%; Score 173; DB 10; Length 691;
Best Local Similarity 63.8%; Pred. No. 1,1e-38;
Matches 279; Conservative 0; Mismatches 155; Indels 3; Gaps 1;

OY 400 TCTGGCAAGTGTTCACAACTGCTTATTTGGATTGTGTAAGCTTTGCACTGAGCT 459
DB 168 TCTGGCAAGTGTTCACAACTGCTTATTTGGATTGTGTAAGCTTTGCACTGAGCT 227
OY 460 GGAAGAAGCTTCTGCACTGCTTCTGTTGACACCTGTCCTCAATGATCTCTTATTA 519
DB 228 GGCAGAGCCAAAGTCAAGCCGCTGCTTGTGATGACAAAAGAACACCCATCAT 287
OY 520 GATGCCAAGCTCAAGAGTGTGT---AAGCGTGAATAGGTTTCAATGTAACAAAC 576
DB 288 AACCTGAAGCCGTCAAGAGTGTGTGAAGAGTGTGTGCTTGTGTTGATCACTAC 347
OY 577 CAACCTGGGCTGCAAGAGTGTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 636
DB 348 TCCCTTGGGCTGCAAGAGTGTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 407
OY 637 TCCAGAGAGCTGATGATGTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 696
DB 408 GGCAGTGAAGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 467
OY 697 TCTGAAAAGAGATGTTGTTCAAGTTACCAACACCGTGGCGATTAGGCTTAACAC 756
DB 468 AAGGAAAAGAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 527
OY 757 TTTGATTGCAAGTGGCGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTG 816
DB 528 TTTGACCTTATGATGCGCGCGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTG 587
OY 817 GCGGCTTCCCAATGATG 833
DB 588 GCGAAGCTCCTCGGTGG 604

RESULT 2

BI200729 450 bp mRNA linear EST 10-JUN-2001
LOCUS o1f05fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
DEFINITION library Fusarium sporotrichioides cDNA clone o1f05fs 5', mRNA
sequence.
ACCESSION BI200729
VERSION BI200729.1 GI:14666701
KEYWORDS EST.
SOURCE Fusarium sporotrichioides.
ORGANISM Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE 1 (bases 1 to 450)
AUTHORS Ren,Q., Isg,A., Fedlow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broeou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broeou.edu
Contact Dr. Marian Beremand regarding clone availability. Included
is the best homolog from a blastx search of Genbank nr 04-09-01
633 5e-66 g11170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE
KRECURSOR (EN
Seq primer: T3
High quality sequence stop: 440.

FEATURES

source

1..450
Location/Qualifiers
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db xref="taxon:5514"
/clone="o1f05fs"
/clone.lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT

90 a 125 c 102 g 133 t

ORIGIN

Query Match 12.0%; Score 122.2; DB 13; Length 450;
Best Local Similarity 63.6%; Pred. No. 4e-24;
Matches 203; Conservative 0; Mismatches 113; Indels 3; Gaps 1;

OY 400 TCTGGCAAGTGTTCACAACTGCTTATTTGGATTGTGTAAGCTTTGCACTGAGCT 459
DB 132 TCTGGCAAGTGTTCACAACTGCTTATTTGGATTGTGTAAGCTTTGCACTGAGCT 191
OY 460 GGAAGAAGCTTCTGCACTGCTTCTGTTGACACCTGTCCTCAATGATCTCTTATTA 519
DB 192 GGCAGAGCCAAAGTCAAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 251
OY 520 GATGCCAAGCTCAAGAGTGTGT---CGGTGAATGTTTCAATGTAACAAAC 576
DB 252 AACCTGAAGCCGTCAAGAGTGTGTGAAGAGTGTGTGCTTATGCTTACCACTAC 311
OY 577 CAACCTGGGCTGCAAGATGATGCTGCTTACGTTTGGCTGCTGCTGCTGCTGCTG 636
DB 312 TCCCGTGGGCTGCAAGAGTGTGTGCTTACGTTTGGCTGCTGCTGCTGCTGCTG 371
OY 637 TCCAGAGAGCTGATGATGTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 696
DB 372 GGTATGAGGCGAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 431
OY 697 TCTGAAAAGAGATGTTG 715
DB 432 AAGGCAAGAGATGATTTG 450

RESULT 3

BI190695 444 bp mRNA linear EST 10-JUN-2001
LOCUS i3g10fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
DEFINITION library Fusarium sporotrichioides cDNA clone i3g10fs 5', mRNA
sequence.
ACCESSION BI190695
VERSION BI190695.1 GI:14664374
KEYWORDS EST.
SOURCE Fusarium sporotrichioides.
ORGANISM Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

REFERENCE B1187295
 TITLE JOURNAL
 COMMENT

Hypocretales; mitosporic Hypocretales; Fusarium.
 1 (bases 1 to 444)
 Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand
 'M. and Roe, B.
 Analysis of a Fusarium sporotrichioides EST database
 Unpublished (2001)
 Contact: Bruce A. Roe, University of Oklahoma, broeou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broeou.edu
 Contact Dr. Marian Beremand regarding clone availability. Included
 is the best homolog from a blastx search of Genbank nr 04-09-01
 576 36-59 g|1170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE
 KPRECURSOR (EN
 Seq primer: T3.
 Location/Qualifiers
 1..444
 /organism="Fusarium sporotrichioides"
 /strain="Tri 10"
 /db_xref="taxon:5514"
 /clone="13910f8"
 /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
 cDNA library"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
 XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
 ; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 85 a 127 c 92 g 140 t
 ORIGIN

Query Match 10.9%; Score 111; DB 13; Length 444;
 Best Local Similarity 64.1%; Pred. No. 6.8e-21;
 Matches 184; Conservative 0; Mismatches 100; Indels 3; Gaps 1;

Oy 400 TCTGGAGTGGTTCACAACTCGTTATGGATTGTTAAAGCTTCTTGACAGTGGCT 459
 |||||
 Db 158 TCTGGAGTGGCCACTCTACTCGATCTGGAGCTGCTCAACCTTCTTGCTTTGGAGC 217
 |||||
 Oy 460 GGAAGAGCTTCTGCTCATGCTGCTGTTGACACCTGCTGCCCAATGATCTCTTTATTA 519
 |||||
 Db 218 GCGAAGGCTAAAGTCAGCGCCCTGCTGCTGATGACCAAGATTAACCTATATCACT 277
 |||||
 Oy 520 GATGCCAATGCTCAAGTGTGTTGA---CGGTGTAATGGTTTCATGTTGAACAACAAC 576
 |||||
 Db 278 AACCTGAACGCTGTCACAGGTTGAGGGGTGCTGCTTATGCTTGACCAACTAC 337
 |||||
 Oy 577 CAACCTGGGCTGTCATATGATGAGCTGCTTACGGTTGCGGCTGCTTATTTGCTGGC 636
 |||||
 Db 338 TCCCGTGGGCTGTCACAGACGACCTTGCCTTACGGTTTGGCTTACCAAGCTTGCTGT 397
 |||||
 Oy 637 TCCACGAGAGCTGATGATGTTGGCTGTTATGTAATGACCTTAC 683
 |||||
 Db 398 GGTAGTAGGCGCAGCTGTGCTGCTGCTATGCTTCACTTAC 444
 |||||

RESULT 4
 B1187295 426 bp mRNA linear EST 10-JUL-2001
 LOCUS B1187295
 DEFINITION B1187295.1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
 library Fusarium sporotrichioides cDNA clone ah11f5 5', mRNA
 sequence.
 ACCESSION B1187295
 VERSION B1187295.1
 KEYWORDS GI:14660974
 SOURCE EST.
 ORGANISM Fusarium sporotrichioides.
 Fusarium sporotrichioides.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocretales; mitosporic Hypocretales; Fusarium.
 REFERENCE 1 (bases 1 to 426)
 Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand
 'M. and Roe, B.

TITLE JOURNAL
 COMMENT

Analysis of a Fusarium sporotrichioides EST database
 Unpublished (2001)
 Other ESTs: ah11f5.f1
 Contact: Bruce A. Roe, University of Oklahoma, broeou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broeou.edu
 Contact Dr. Marian Beremand regarding clone availability. Included
 is the best homolog from a blastx search of Genbank nr 04-09-01
 565 5e-58 g|1170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE
 KPRECURSOR (EN
 Seq primer: T3
 High quality sequence stop: 338.
 Location/Qualifiers
 1..426
 /organism="Fusarium sporotrichioides"
 /strain="Tri 10"
 /db_xref="taxon:5514"
 /clone="ah11f5"
 /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
 cDNA library"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
 XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
 ; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 82 a 119 c 91 g 134 t
 ORIGIN

Query Match 10.3%; Score 104.4; DB 13; Length 426;
 Best Local Similarity 63.9%; Pred. No. 5.3e-19;
 Matches 175; Conservative 0; Mismatches 96; Indels 3; Gaps 1;

Oy 400 TCTGGAGTGGTTCACAACTCGTTATGGATTGTTAAAGCTTCTTGACAGTGGCT 459
 |||||
 Db 148 TCTGGAGTGGCCACTCTACTCGATCTGGAGCTGCTCAACCTTCTTGCTTTGGAGC 207
 |||||
 Oy 460 GGAAGAGCTTCTGCTCATGCTGCTGTTGACACCTGCTGCCCAATGATCTCTTTATTA 519
 |||||
 Db 208 GCGAAGGCTAAAGTCAGCGCCCTGCTGCTGATGACCAAGATTAACCTATATCACT 267
 |||||
 Oy 520 GATGCCAATGCTCAAGTGTGTTGA---CGGTGTAATGGTTTCATGTTGAACAACAAC 576
 |||||
 Db 268 AACCTGAACGCTGTCACAGGTTGAGGGGTGCTGCTTATGCTTGACCAACTAC 327
 |||||
 Oy 577 CAACCTGGGCTGTCATATGATGAGCTGCTTACGGTTGCGGCTGCTTATTTGCTGGC 636
 |||||
 Db 328 TCCCGTGGGCTGTCACAGACGACCTTGCCTTACGGTTTGGCTTACCAAGCTTGCTGT 387
 |||||
 Oy 637 TCCACGAGAGCTGATGATGTTGGCTGTTATGTAATGACCTTAC 670
 |||||
 Db 388 GGTAGTAGGCGCAGCTGTGCTGCTGCTATGCTTCACTTAC 421
 |||||

RESULT 5
 B1190568 215 bp mRNA linear EST 10-JUL-2001
 LOCUS B1190568
 DEFINITION B1190568.1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
 library Fusarium sporotrichioides cDNA clone 12e11f5 5', mRNA
 sequence.
 ACCESSION B1190568
 VERSION B1190568.1
 KEYWORDS GI:14664247
 SOURCE EST.
 ORGANISM Fusarium sporotrichioides.
 Fusarium sporotrichioides.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocretales; mitosporic Hypocretales; Fusarium.
 REFERENCE 1 (bases 1 to 215)
 Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand
 'M. and Roe, B.
 Analysis of a Fusarium sporotrichioides EST database
 Unpublished (2001)

JOURNAL

Submitted (29-SEP-2000) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. UK Email:

COMMENT

biohelp@hmp.mrc.ac.uk
Vector: pBluescript II KS
V type: phagemid
Primer: KS

FEATURES

source

One pass dye-terminator sequencing of BAC (pBelobACII) cloned genomic sequence
The BACs can be obtained from <http://www.inkycy.com>.
Location/Qualifiers

BASE COUNT 128 a 163 c 45 g 158 t
ORIGIN

Query Match 7.1%; Score 72; DB 17; Length 494;
Best Local Similarity 50.3%; Pred. No. 1.3e-09;
Matches 177; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

207 TGTGTGTAACGCTAGACAGACCAAGACATCTACCAAGATCTACTACACCGCCAA 266
119 TGTCTTACTACTGCTACTACTACAGAGCTGCTACTACTCTGCTACTACTACTAC 178
267 GGTCTACTCTACTCTGCTACCAAGACAGTAAACCAAGCACTACCAAGCACTACCA 326
179 TACTACTACTACTCTGCTACTACTACTACTACTACTACTACTACTACTACTACTAC 238
327 GACTAGCACTACTGCGCGTCTCTACTCTCCACCGCTCTCTGCTGCTGTAACAGTCAT 386
239 TACTACTACTACTCTACTACTACTACTACTACTACTACTACTACTACTACTACTGCTAC 298
387 CTCTGGCGGTAAATCTGCGAGTGTTCACAACCTGTTATTTGAGATTGTTGAAAGCTTC 446
299 TACTACTGCTACTACTACTACTACTACTACTACTACTGCTGCTGCTACTGCTGCTAC 358
447 TTGCAAGCTGCTGGAAGGCTTCTGTCAGCTGCTGTTGACACCTGCTGCTGCTGCTAC 506
359 TAC 418
507 TATCTCTTATTAAGTCCAAAGCTCAAGTGTGTAAGCGTGGTAAATGCT 558
419 TACTACTACTGCTGCTACTACTACTACTACTACTACTACTACTACTACTACTGCT 470

RESULT 8
BH879665 350 bp DNA linear GSS 05-AUG-2002
LOCUS

DEFINITION h47h12.g1 WGS-2maysf (JM107 adapted methyl filtered) Zea mays
genomic clone h47h12.5', DNA sequence.

ACCESSION BH879665
VERSION BH879665.1 GI:22115562
KEYWORDS GSS.

SOURCE

ORGANISM

Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS

Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Muller, S., Nascentino, L., Zuber, T., McCombie, W.R. and Martienssen, R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
Contact: W. Richard McCombie
Lila Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874

COMMENT

Email: mccombie@cshl.org
Plate: h47 row: h column: 12
Seq primer: -21M13univFwd
Class: shotgun
High quality sequence stop: 350.
Location/Qualifiers

FEATURES

source

One pass dye-terminator sequencing of cosmid cloned genomic
Query Match 7.0%; Score 70.8; DB 17; Length 350;
Best Local Similarity 53.2%; Pred. No. 2.4e-09;
Matches 150; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

199 AGTAAATGCTGTAAAGCTAGACAGACCAAGACATCTACCAAGATCTACTAC 258
49 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 108
259 ACCGCCAAGCTATGCTACTCTGACCAAGACAGTAAACCAAGACATCTACCAAGACA 318
109 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 168
319 ACTACCAAGCTAGCACTACTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 378
169 AGCACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 228
379 AAGGTACTCTGCGGTAAATCTGCGAGTGTTCACAACCTGTTATTTGAGATTGTTGT 438
229 ACT 288
439 AAAGCTCTTGCAAGCTGCGCTGGAAGCTTCTCTCACTGCT 480
289 ACTACTACTAGTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 330

RESULT 9

LOCUS

FR0025683 450 bp DNA linear GSS 10-DEC-1997
DEFINITION F.rubripes GSS sequence, clone 154E17a12, genomic survey sequence.

ACCESSION AL018519
VERSION AL018519.1 GI:2684887
KEYWORDS GSS: genome survey sequence.

SOURCE

ORGANISM

Takifugu rubripes.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Takifugu.

1 (bases 1 to 450)

REFERENCE

AUTHORS

Elgar, G., Clark, M., Smith, S., Week, S., Warner, S., Umranta, Y., Williams, G. and Brenner, S.
Direct Submission
Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hmp.mrc.ac.uk
Vector: pBluescript II KS
V type: phagemid
Primer: KS

COMMENT

One pass dye-terminator sequencing of cosmid cloned genomic

BASE COUNT 210 a 208 c 107 g 387 t 2 others
 DH10B[®]
 ORIGIN

Query Match 6.9%; Score 70; DB 17; Length 914;
 Best Local Similarity 48.7%; Pred. No. 7.5e-09;
 Matches 190; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

199 AGTAACATGCTGGTAACGCTAGACGACCAAGACATCTACCAAGATCTACTACC 258
 Db ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 228
 Qy ACCGCCAAGCTACTGCTACTGTCACCAAGACAGTAACCAAGACCAAGACCA 318
 Db ACCGCACTACTACTACTGCACTACTACTACTACTACTACTACTACTACTACT 288
 Qy ACTACCAAGACTACTACTGCGCTGCTCTCACTTCCACTCTTCTTCTGCTGTTAC 378
 Db ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 348
 Qy AAGTCATCTCTGCGGTAATCTGGAGTGTCCCAACTCGTTATGGATTTGT 438
 Db ACTGTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 408
 Qy AAGCTTCTGCACTGCGCTGGAAGCTTCTGCTACTGCTGTTGACACCTGTGCC 498
 Db ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 468
 Qy TCCAAAGTATCTTTTATTAGATGCCAAGCTCAAGGTGTGAAGGTGTATGT 558
 Db ACTAATGTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 528
 Qy TTCAATGTGATCAACACCAACCTTGGCT 588
 Db TTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 558

RESULT 12
 AZ204694 933 bp DNA linear GSS 31-AUG-2000
 LOCUS
 DEFINITION SP_0100_A1.G12.SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=100 Col=23 Row=M, DNA sequence.

ACCESSION AZ204694 GI:8399614
 VERSION
 KEYWORDS GSS.
 SOURCE Strongylocentrotus purpuratus.
 ORGANISM Strongylocentrotus purpuratus
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 Echinoidea; Euechinoidea; Echinoidae; Echinoidae;
 Strongylocentrotidae; Strongylocentrotus.

REFERENCE 1 (bases 1 to 933)
 AUTHORS Cameron,R.A., Mahatras,G., Raet,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Pousetka,A.J., Livingston,B.T., Wray,G.A., Ertensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and Hood,L.
 TITLE A sea urchin genome project: Sequence scan, virtual map, and additional resources
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
 MEDLINE 20402566
 COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L
 Division of Biology 156-29
 California Institute of Technology
 Pasadena California 91125, USA
 Tel: (626) 395-8421
 Fax: (626) 793-3047
 Email: acameron@caltech.edu
 Plate: 100 row: M column: 23
 Seg primer: SP6
 Class: BAC ends
 High quality sequence stop: 933.
 Location/Qualifiers
 1..933

FEATURES
 source

/organism="Strongylocentrotus purpuratus"
 /db_xref="taxon:7668"
 /clone="plate=100 Col=23 Row=M"
 /clone_1b="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
 /note="Organ: sperm; Vector: BAC3.6; BAC Clones in E-Coli DH10B"
 BASE COUNT 226 a 235 c 156 g 316 t
 ORIGIN

Query Match 6.8%; Score 69.6; DB 17; Length 933;
 Best Local Similarity 48.9%; Pred. No. 9.9e-09;
 Matches 186; Conservative 0; Mismatches 194; Indels 0; Gaps 0;

189 CGATGCCAAGTAACATGCTGTAACGCTAGACGACCAAGACATCTACCAAGAC 248
 Db CGCATACACCGGTAATCTACTACTACTACTACTACTACTACTACTACTACTACT 169
 Qy ATCTACTACACCGGCAAGCTACTGTCACCAAGACAGTAACCAAGACCAAC 308
 Db TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 229
 Qy TACCAAGACACTACCAAGCTACTGCGCTGCTTCACTTCCACTCTTCTTC 368
 Db CACCACTACTACTACTTCCACTTATTACTACTACTACTACTACTACTACTACTACT 289
 Qy TCGTGTAGAGTCACTCTGCGGTAATCTGGAGTGTCCCAACTCGTTATTTG 428
 Db TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 349
 Qy GATTTGTTGAAGCTTCTGCACTGCGCTGGAAGCTTCTGCTACTGCTGTTGA 488
 Db TGCAATTAATTACTACTACTTCTACTACTACTACTACTACTACTACTACTACTACT 409
 Qy CACCTGCTCCCAAGTATCTTTTATTAGATGCCAAGCTCAAGGTGTGAACG 548
 Db TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 469
 Qy TCGTAATGTTTCAATGTTA 568
 Db TAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 489

RESULT 13
 AZ183942 788 bp DNA linear GSS 30-AUG-2000
 LOCUS
 DEFINITION SP_1002_A1.H11.SP6 Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=1002 Col=21 Row=O, DNA sequence.

ACCESSION AZ183942 GI:8356317
 VERSION
 KEYWORDS GSS.
 SOURCE Strongylocentrotus purpuratus.
 ORGANISM Strongylocentrotus purpuratus
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 Echinoidea; Euechinoidea; Echinoidae; Echinoidae;
 Strongylocentrotidae; Strongylocentrotus.

REFERENCE 1 (bases 1 to 788)
 AUTHORS Cameron,R.A., Mahatras,G., Raet,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Pousetka,A.J., Livingston,B.T., Wray,G.A., Ertensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and Hood,L.
 TITLE A sea urchin genome project: Sequence scan, virtual map, and additional resources
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
 MEDLINE 20402566
 COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L
 Division of Biology 156-29
 California Institute of Technology
 Pasadena California 91125, USA
 Tel: (626) 395-8421
 Fax: (626) 793-3047
 Email: acameron@caltech.edu

FEATURES
 source

Plate: 1002 row: 0 column: 21
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 788.
Location/Qualifiers

FEATURES
source
1. 788
/organism="Strongylocentrotus purpuratus"
/db_xref="taxon:7668"
/clone="Plate=1002 Col=21 Row=0"
/clone_11b="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACs 6; BAC Clones in E-Coli DH10B"

BASE COUNT
248 a 183 c 98 g 259 t

Query Match
Best Local Similarity 52.7%; Pred. No. 2.9e-08;
Matches 147; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 199 AGTAAATGCTGTGTAACGTACGACGACCAAGAAACATTCACCAAGCATCTACTACC 258
DB 357 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 416
QY 259 ACCGCAAGGCTACTGCTACTGCTACGACCAAGACAGTAACCAAGCACTACTACCAAGCA 318
DB 417 ACT 476
QY 319 ACTACCAAGTACGACGCTACTGCGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 378
DB 477 ACT 536
QY 379 AAGGTATCTTCGCGGTAAATCTGGAGAGGTTTCAACAACGTGATTTGGATTTGTTGT 438
DB 537 ACGTTTATTAATACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 596
QY 439 AAAGCTTCTTGACGCTGCGCTGGAAAAAGCTTCTGTCACT 477
DB 597 ACT 635

RESULT 14
BH179321/c 627 bp DNA linear GSS 19-OCT-2001
LOCUS 014 P.01-21 SMBAC1 Schistosoma mansoni genomic clone 014P01 5', DNA
DEFINITION
ACCESSION BH179321
VERSION BH179321.1 GI:16280048
KEYWORDS GSS.
SOURCE Schistosoma mansoni.
ORGANISM Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.

REFERENCE
AUTHORS Le Paslier, M.-C., Pierce, R.J., Merlin, F., Hirai, H., Wu, W., Williams
1 (bases 1 to 627)
TITLE D.L., Johnston, D., Loverde, P.T. and Le Paslier, D.
Construction and characterization of a Schistosoma mansoni
bacterial/artificial chromosome library
JOURNAL Genomics 65 (2), 87-94 (2000)
MEDLINE 20247247
COMMENT Other GSSes: 014_P_01-rev
Contact: Pierce RJ
INSERM U 167
Institut Pasteur de Lille
1 rue du Professeur A. Calmette, 59019-Lille, France
Tel: (33) (0)3 20877783
Fax: (33) (0)3 20877888
Email: Raymond.Pierce@pasteur-lille.fr
CNS sequencing ID=D00A014CH01CPI
Plate: 014 row: P column: 01
Seq primer: M13 -21 primer
Class: BAC ends
High quality sequence stop: 627.

FEATURES
source
Location/Qualifiers

1. 627
/organism="Schistosoma mansoni"
/strain="Puerto-Rican"
/db_xref="taxon:6183"
/clone="014P01"
/clone_11b="SMBAC1"
/sex="mixed"
/dev_stage="cercariae"
/lab_host="Biomphalaria glabrata"
/note="Vector: pBelOBAC 11; Site 1: Hind III; Partially
Hind III digested and size-selected S. mansoni cercarial
DNA was ligated into Hind III digested pBelOBAC 11 vector
and used to transform E. coli DH10B. The complete library
contains 23808 clones from 4 independent
sizing-ligation-transformations. Average insert size
ranges from 70-127 kb and genome coverage is 7.9-fold."

BASE COUNT
169 a 79 c 196 g 167 t 16 others

Query Match
Best Local Similarity 52.3%; Pred. No. 3.8e-08;
Matches 135; Conservative 5; Mismatches 118; Indels 0; Gaps 0;

QY 226 ACCAAGAACATCTACCAAGACATCTACTACCAAGCGCAAGCTACTGTCTACACC 285
DB 398 ACGATTACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 339
QY 286 ACCAAGAACATCTACCAAGACATCTACTACCAAGCGCAAGCTACTGTCTACACC 345
DB 338 ACT 279
QY 346 GCTTCTACTTCCACCTTCTTCTTCTGCTGTACAGGTATCTTGGCGGTAATCTGGC 405
DB 278 ACT 219
QY 406 AGTGTTCACCAACTCTGTTATTTGGATTTGTTAAACCTCTTGACCTGACCTGAAAA 465
DB 218 ATTCTACTACMCCTACTGSSCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 159
QY 466 GCTTCTGCTACTGCTGCT 483
DB 158 AACCTGCTACTGCTACT 141

RESULT 15
CNS07LFL/c 627 bp DNA linear GSS 08-OCT-2001
LOCUS T7 end of clone 014CH01 of library SMBAC1 from strain Puerto-Rican
DEFINITION
ACCESSION CNS07LFL
VERSION AL616275
KEYWORDS AL616275.1 GI:16029499
SOURCE Schistosoma mansoni.
ORGANISM Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.

REFERENCE
AUTHORS Le Paslier, M.-C., Pierce, R.J., Merlin, F., Hirai, H., Wu, W.,
1 (bases 1 to 627)
TITLE Williams, D.L., Johnston, D., Loverde, P.T. and Le Paslier, D.
Construction and characterization of a Schistosoma mansoni
bacterial artificial chromosome library
JOURNAL Genomics 65 (2), 87-94 (2000)
MEDLINE 20247247
COMMENT Direct SubMISSION
Genoscope.
Submitted (05-OCT-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
DNA was ligated into Hind III digested pBelOBAC 11 vector and used

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

to transform E. coli DH10B. The complete library contains 23808 clones from 4 independent sizing-ligation-transformations. Average insert size ranges from 70-127 kb and genome coverage is 7.9-fold.

FEATURES

source

Location/Qualifiers

1..627

/organism="Schistosoma mansoni"

/strain="Puerto-Rican"

/db_xref="taxon:6183"

/clone="014CH01"

/clone_lib="SMBAC1"

/note="end : 17"

BASE COUNT 169 a 79 c 196 g 167 t 16 others

ORIGIN

Query Match

Best Local Similarity 52.3%; Score 67.2; DB 17; Length 627;

Matches 135; Conservative 5; Mismatches 118; Indels 0; Gaps 0;

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QY 226 ACCAAGAAGCATCTACCAAGACATCTACTACCAAGCAAGCTACTGTCTACTGTCACC 285
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Db 398 ACGATTACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 339
    |||||
QY 286 ACCAAGACATACCAAGACATACCAAGACATACCAAGACATACCAAGACATACCAAGAC 345
    |||||
Db 338 ACTCTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 279
    |||||
QY 346 GCTTCTACTTCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 405
    |||||
Db 278 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 219
    |||||
QY 406 AGTGTTCACACTCGTTATGATGTTGTAAGCTCTTGACGCTGGCTGGAAGA 465
    |||||
Db 218 ATTCTACTACMCCTACTGSSCTTCTTCTCTACTATTCTTAAACCTGTACTACMCMA 159
    |||||
QY 466 GCTTCTGCTACTGCTCT 483
    |||||
Db 158 AACCTGTCTACTGCTACT 141
    |||||
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Job time : 1373.68 secs

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